Report of the 3rd International Congress of Virology

Not having attended the previous international congresses of virology, I was pleasantly surprised to find a generally high level of scientific discourse, with mounting evidence that plant and animal virologists are approaching the levels of genetic and biochemical sophistication formerly the province of bacterial virologists. Having recently attended the Gordon Conference on Animal Cells and Viruses, I naturally heard a good deal of material for the second time on this occasion. My report will focus particularly on items which were at least partially new to me.

The conference was divided into symposia (the only item on the morning schedule), workshops (six per each of two afternoon sessions), and conversations (or "poster sessions," open throughout the day). Talks at the symposia tended, quite rightly, to summarize results over several years, but a number of particularly interesting items emerged. The deletion mutants of SV 40 (discussed by Nathans & Brockman in two symposia and obtained from high multiplicity passage stocks by complementation of ts mutants) now include deletions in the region of termination of replication (proving there is no signal for termination) and in large regions of the late genes (these mutants can still transform cells). The ribosomal binding site for a species of brome mosiac virus RNA has been determined by Kaesberg et al. and has several interesting features, particularly its great proximity to the 5' end (there are only 12 bases from the methylated blocked end to the structural gene), and its high content of A and U. The last day's symposium included promising (although unfinished) efforts to link defective interfering (DI) particles of VSV (Huang), herpes virus (Ben Porat), and lymphocytic choriomeningitis virus (Welsh) to persistent infections: in all cases, cyclic growth of wild type and DI virus, the mechanism of interference, and the nature of the DI virus are under study. Viruses likely to be direct analogues of DI animal viruses have now been identified among plant viruses as well (Schneider, satellite virus of tobacco necrosis virus). In the symposium in which I and my colleague, J.M. Bishop, presented papers, there were several items of interest: Winocour's evidence that SV 40 prefers some integration sites during lytic infection, but clearly uses more than one (Brockman & Nathans agree); his demonstration that an SV 40 mutant can recombine with viral DNA integrated in UV-irradiated virus - transformed monkey cells; Steiner's mounting evidence that cell transformation may be linked in an interesting way to failure of maturation of certain fucolipids; Weiss' report that the putative human leukemia agent may contain an (unexplained) component ressembling the endogenous baboon virus, as well as the component ressembling the simian sarcoma virus; the failure of his group to detect DNA homologous to viral RNA in the starting leukemic cells casts considerable doubt upon the role of this virus in the etiology of human leukemia, despite much suggestive evidence in favor.

The workshops generally consisted of a rapid series of relatively short papers, with insufficient time for discussion. Nevertheless, several were notable. In the poliovirus session, Fellner & Wimmer have used RNA "fingerprinting" techniques to study genomic RNA's: all strains can be readily distinguished by these techniques and long tracts of poly rC can be identified. Fellner has sequenced the ribosome binding site for EMC RNA, and Wimmer has evidence that the poly A of polio RNA is templated by poly U. The sequence of assembly of procapsid → provirion → virion is known in outline, but some precursor-product relationships are uncertain, and it is not clear how viral RNA gets inside the protein shell. It is now agreed that mengovirus RNA has a

short stretch of poly A required for infection at the 3' terminus (Burness). Baltimore claimed that partial uncoating of polio virions could be performed by plasma membrane preparations and nascent cleavage of polio polyprotein by extracts of uninfected cells.

In a genetics workshop, Vogt presented evidence for relatively stable heterozygotes of avian RNA tumor viruses and described the conditions which favor appearance of transformation-defective deletion mutants. Stephenson described several mutants of MuLV - at least one with a lesion in reverse transcriptase and one with a defect in processing a viral polyprotein - and Fields presented biochemical characterization of ts mutants of reovirus. Pringle showed that five of the six complementation groups of VSV mutants could be assigned a known viral protein. Sugiura's results suggested that the influenza deletion mutants (von Magnus phenomenon) could be located in single complementation group (I) defined by ts mutants.

In the integration workshop (in which I spoke), Gottesman described an elegant in vitro system for studying excision of lambda DNA. Baczko showed that as much as 100,000 copies of adenovirus DNA was present per infected cell and that some may be integrated (by restriction enzyme tests) early in the life cycle. Nonoyama still can't decide whether any Ebstein Barr virus DNA is integrated (though he appears not to see the circular EBV DNA so clearly shown by Lindahl). Baluda claimed that infrequently expressed avian tumor virus DNA was integrated adjacent to reiterated cell sequences, and highly expressed DNA next to unique sequences only. Little was new with endogenous viruses, but Bentvelzen claimed that he had induced a virulent mammary tumor virus from C3Hf mice; this could be very significant if it proves to be identical to the milk borne agent, MMTV-S. Other sessions I attended were not worth reporting on.

I did not engage in many "conversations" (many of these seemed rather clinical), but one provocative display (Hagemann) suggested that a tumor virus might be implicated in mammary cancer in several rat strains.

Of course, it is not possible to detail here the most important encounters at a meeting of this sort - discussions with far flung virologists, in my own field and others. I am grateful for the opportunity to have participated.

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